



SEQUENCE LISTING

<110> Wilkins, Thea A.
The Regents of the University of California

<120> Cotton Transcription Factors and Their Uses

<130> 023070-095600US

<140> US 09/453,387

<141> 1999-12-02

<160> 26

<170> PatentIn Ver. 2.1

<210> 1

<211> 1006

<212> DNA

<213> Gossypium hirsutum

<220>

<221> CDS

<222> (59) .. (943)

<223> GhMYB1

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Met Gly Arg Ser Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala
1 5 10 15

tgg acc aaa gag gaa gat caa cgc ctc atc aac tac atc cgt gtc cat 154
Trp Thr Lys Glu Glu Asp Gln Arg Leu Ile Asn Tyr Ile Arg Val His
20 25 30

ggt gaa ggc tgc tgg cgt tcc ctc ccc aaa gct gct ggg ctg ctt aga 202
Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
35 40 45

tgt ggt aag agt tgc aga tta aga tgg ata aac tac ttg agg cct gat 250
Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

ctt aag aga gga aat ttc act gaa gaa gaa gat gag ctt atc atc aag 298
Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

ctt cac agt tta ctt gga aac aaa tgg tca ttg att gct gga aga tta 346
Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

cca gga aga aca gat aat gag ata aag aac tac tgg aac aca cac atc 394
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

aaa aga aag ctt ata agc aga gga att gat cca caa act cat cgt cct 442
Lys Arg Lys Leu Ile Ser Arg Gly Ile Asp Pro Gln Thr His Arg Pro
115 120 125

ctc aat caa acg gcc aat acc aac aca gtc aca gcc ccc acc gaa ttg 490
 Leu Asn Gln Thr Ala Asn Thr Asn Thr Val Thr Ala Pro Thr Glu Leu
 130 135 140
 gat ttc aga aac tcg ccc aca tcc gtt tcc aaa tcc agt tcc atc aaa 538
 Asp Phe Arg Asn Ser Pro Thr Ser Val Ser Lys Ser Ser Ser Ile Lys
 145 150 155 160
 aac ccg tct ctg gat ttc aat tac aat gaa ttt caa ttc aag tcc aac 586
 Asn Pro Ser Leu Asp Phe Asn Tyr Asn Glu Phe Gln Phe Lys Ser Asn
 165 170 175
 aca gat tcc ctt gaa gaa ccc aac tgt aca gcc agc agt ggc atg act 634
 Thr Asp Ser Leu Glu Glu Pro Asn Cys Thr Ala Ser Ser Gly Met Thr
 180 185 190
 aca gat gaa gag caa caa gaa cag ctg cac aag aag cag caa tac ggt 682
 Thr Asp Glu Glu Gln Gln Glu Gln Leu His Lys Lys Gln Gln Tyr Gly
 195 200 205
 ccg agc aat ggg caa gac ata aat ttg gag ctg tcg att ggg att gtt 730
 Pro Ser Asn Gly Gln Asp Ile Asn Leu Glu Leu Ser Ile Gly Ile Val
 210 215 220
 tca gct gac tca tct cgg gta tca aat gcc aac tcg gcc gag tcg aaa 778
 Ser Ala Asp Ser Ser Arg Val Ser Asn Ala Asn Ser Ala Glu Ser Lys
 225 230 235 240
 cca aag gta gat aac aac aat ttc cag ttt ctt gaa caa gct atg gtg 826
 Pro Lys Val Asp Asn Asn Asn Phe Gln Phe Leu Glu Gln Ala Met Val
 245 250 255
 gct aag gcg gta tgt ttg tgt tgg caa tta ggt ttt gga aca agt gaa 874
 Ala Lys Ala Val Cys Leu Cys Trp Gln Leu Gly Phe Gly Thr Ser Glu
 260 265 270
 att tgt agg aac tgt caa aat tca aat tca aat ggc ttc tat agt tat 922
 Ile Cys Arg Asn Cys Gln Asn Ser Asn Ser Asn Gly Phe Tyr Ser Tyr
 275 280 285
 tgt aga ccc ttg gat tca tag ggatcatcttt ttcttctttt tttctgtttt 973
 Cys Arg Pro Leu Asp Ser
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<210> 2
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 <213> Gossypium hirsutum

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 20 25 30
 Gly Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg
 35 40 45
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

cca gat atc aaa cgt ggt aac ttt gct caa gac gaa gag gac tta att	302
Pro Asp Ile Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile	
65 70 75	
atc aaa ctc cat gct ctc ctt ggt aac cgg tgg tca ctg ata gct ggt	350
Ile Lys Leu His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly	
80 85 90	
aga tta cca gga aga aca gat aat gaa gtg aag aac tat tgg aat tcc	398
Arg Leu Pro Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser	
95 100 105	
cat ata aag aga aag cta atg aag atg ggg atc gat cct aat aac cat	446
His Ile Lys Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His	
110 115 120 125	
aag ttg aac caa tat cct cat cat gtt ggt ccc ctt aac ccc acc acc	494
Lys Leu Asn Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr	
130 135 140	
acc aac tcc atg gat gtg gca tgt aag ctt aga gtg tgt tca aca gac	542
Thr Asn Ser Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp	
145 150 155	
aat gat gat ggg atc tca gat gct gca agt tat ctc gaa gac gca aca	590
Asn Asp Asp Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr	
160 165 170	
ccg ccc act ggt ata tcc aac ttg gac ctt gat ctc aca att gct ttt	638
Pro Pro Thr Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe	
175 180 185	
cct tcg agt cct atc aag aat att att gaa gaa agc cag cag aaa aca	686
Pro Ser Ser Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr	
190 195 200 205	
gca tct att gta aca aat gat gaa gaa gaa caa tat aca gtc cct acc	734
Ala Ser Ile Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr	
210 215 220	
ctt ctt ctt ttc aga tga gacaaaaaaaaa aaagcctcac acatgtggag	782
Leu Leu Leu Phe Arg	
225	
attcgtgcaa aagacctaaa ggcttacgaa ggcaacatgc acgccattgt caaattcttt	842
tggtatgatgg attgaaacca tatecttgct cattagaaag gaggaagata agctaaaact	902
gtattattgt gtataaattt ggtagaaaga aagatttcaa cttaagaatt aggatcaaat	962
aactgaatga atgaacgaat tgcagataag ttgttaggag gttttcaatc aacttatctg	1022
caattaattt ggtggagctg atgtaggatg atgagttcat cgtacatgaa ctgaaccttt	1082
gatatttcag gctctaattg tctgtttgta tgcgtaaaga tattcttcaa tgtgagatca	1142
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<210> 4
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 <213> Gossypium hirsutum

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 Ser Lys Gln Glu Asp Gln Lys Leu Ile Asp Tyr Ile Arg Ile His Gly
 20 25 30
 Glu Gly Cys Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu His Arg Cys
 35 40 45
 Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Ile
 50 55 60
 Lys Arg Gly Asn Phe Ala Gln Asp Glu Glu Asp Leu Ile Ile Lys Leu
 65 70 75 80
 His Ala Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro
 85 90 95
 Gly Arg Thr Asp Asn Glu Val Lys Asn Tyr Trp Asn Ser His Ile Lys
 100 105 110
 Arg Lys Leu Met Lys Met Gly Ile Asp Pro Asn Asn His Lys Leu Asn
 115 120 125
 Gln Tyr Pro His His Val Gly Pro Leu Asn Pro Thr Thr Thr Asn Ser
 130 135 140
 Met Asp Val Ala Cys Lys Leu Arg Val Cys Ser Thr Asp Asn Asp Asp
 145 150 155 160
 Gly Ile Ser Asp Ala Ala Ser Tyr Leu Glu Asp Ala Thr Pro Pro Thr
 165 170 175
 Gly Ile Ser Asn Leu Asp Leu Asp Leu Thr Ile Ala Phe Pro Ser Ser
 180 185 190
 Pro Ile Lys Asn Ile Ile Glu Glu Ser Gln Gln Lys Thr Ala Ser Ile
 195 200 205
 Val Thr Asn Asp Glu Glu Glu Gln Tyr Thr Val Pro Thr Leu Leu Leu
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 Phe Arg
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<210> 5
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 <213> Gossypium hirsutum

<220>
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 Met Gly Arg Ser Pro Cys Cys Ser Lys
 1 5
 gaa ggc ctt aac aga gga gct tgg act gct ctt gaa gac aaa att ctt 160
 Glu Gly Leu Asn Arg Gly Ala Trp Thr Ala Leu Glu Asp Lys Ile Leu
 10 15 20 25

aaa gat tat atc	aaa gta cac ggt gaa ggt cgt tgg aga aat ctc ccc	208
Lys Asp Tyr Ile	Lys Val His Gly Glu Gly Arg Trp Arg Asn Leu Pro	
	30 35 40	
aaa aga gct ggt ctt aag aga tgt ggg aaa agt tgt agg ctt cgg tgg	256	
Lys Arg Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp		
	45 50 55	
ttg aat tat ttg aga cct gat att aaa aga ggt aac ata tca cct gac	304	
Leu Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Asn Ile Ser Pro Asp		
	60 65 70	
gag gaa gag ctt atc atc aaa ctc cac aaa ctc ttg gga aac aga tgg	352	
Glu Glu Glu Leu Ile Ile Lys Leu His Lys Leu Leu Gly Asn Arg Trp		
	75 80 85	
tct ttg ata gct ggg agg ctt cca gga cga aca gac aat gaa ata aag	400	
Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys		
	90 95 100 105	
aat tac tgg aac acc aac tta agt aaa aga gtt tcc gat cgt caa aag	448	
Asn Tyr Trp Asn Thr Asn Leu Ser Lys Arg Val Ser Asp Arg Gln Lys		
	110 115 120	
tca ccc gcc gct cct tcg aaa aat ccc gag gcg gct cga cga gga act	496	
Ser Pro Ala Ala Pro Ser Lys Asn Pro Glu Ala Ala Arg Arg Gly Thr		
	125 130 135	
gct ggt aat ggc aat acc aat ggt aat ggt agt ggt agt tcc tcg aca	544	
Ala Gly Asn Gly Asn Thr Asn Gly Asn Gly Ser Gly Ser Ser Ser Thr		
	140 145 150	
cac gtg gtg cgg aca agg gcg aca agg tgc tcc aag gtt ttc ata aac	592	
His Val Val Arg Thr Arg Ala Thr Arg Cys Ser Lys Val Phe Ile Asn		
	155 160 165	
cct cct cac tac aca caa aac aga gac cca aag cct tct tca act tgt	640	
Pro Pro His Tyr Thr Gln Asn Arg Asp Pro Lys Pro Ser Ser Thr Cys		
	170 175 180 185	
tca aat cat ggg gat cac cgg gaa cct aaa aca atg aat gag ttg tta	688	
Ser Asn His Gly Asp His Arg Glu Pro Lys Thr Met Asn Glu Leu Leu		
	190 195 200	
tta ccg ata atg tca gaa tcc gag aat gaa ggg acg acc gat cat ata	736	
Leu Pro Ile Met Ser Glu Ser Glu Asn Glu Gly Thr Thr Asp His Ile		
	205 210 215	
tca tcg gat ttt aca ttt gac ttc aac atg gga gag ttt tgt tta tcg	784	
Ser Ser Asp Phe Thr Phe Asp Phe Asn Met Gly Glu Phe Cys Leu Ser		
	220 225 230	
gat ctt ttg aat tcc gat ttc tgc gat gta aac gag ctt aat tac agc	832	
Asp Leu Leu Asn Ser Asp Phe Cys Asp Val Asn Glu Leu Asn Tyr Ser		
	235 240 245	
aat ggt ttt gat tcg tca ccc tca ccg gat cag cct cct atg gat ttc	880	
Asn Gly Phe Asp Ser Ser Pro Ser Pro Asp Gln Pro Pro Met Asp Phe		
	250 255 260 265	

tcc gac gaa atg cta aaa gag tgg acg gcc gcc gcc tcc act cac tgc 928
 Ser Asp Glu Met Leu Lys Glu Trp Thr Ala Ala Ala Ser Thr His Cys
 270 275 280

tgt cac caa agt gcg gct tcc aat ctc cag tcc ttg cct cca ttt att 976
 Cys His Gln Ser Ala Ala Ser Asn Leu Gln Ser Leu Pro Pro Phe Ile
 285 290 295

gaa aat gga att gaa tga ccttgaaaaa ataaaagacg aaaaatattt 1024
 Glu Asn Gly Ile Glu
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tctcatgtaa actaaataaa cacatcttcc atcattaaaa aaaaaaaaaa aaaaaaa 1081

<210> 6
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 <213> Gossypium hirsutum

<400> 6
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 20 25 30
 Gly Glu Gly Arg Trp Arg Asn Leu Pro Lys Arg Ala Gly Leu Lys Arg
 35 40 45
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro Asp
 50 55 60
 Ile Lys Arg Gly Asn Ile Ser Pro Asp Glu Glu Glu Leu Ile Ile Lys
 65 70 75 80
 Leu His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu
 85 90 95
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr Asn Leu
 100 105 110
 Ser Lys Arg Val Ser Asp Arg Gln Lys Ser Pro Ala Ala Pro Ser Lys
 115 120 125
 Asn Pro Glu Ala Ala Arg Arg Gly Thr Ala Gly Asn Gly Asn Thr Asn
 130 135 140
 Gly Asn Gly Ser Gly Ser Ser Ser Thr His Val Val Arg Thr Arg Ala
 145 150 155 160
 Thr Arg Cys Ser Lys Val Phe Ile Asn Pro Pro His Tyr Thr Gln Asn
 165 170 175
 Arg Asp Pro Lys Pro Ser Ser Thr Cys Ser Asn His Gly Asp His Arg
 180 185 190
 Glu Pro Lys Thr Met Asn Glu Leu Leu Leu Pro Ile Met Ser Glu Ser
 195 200 205
 Glu Asn Glu Gly Thr Thr Asp His Ile Ser Ser Asp Phe Thr Phe Asp
 210 215 220
 Phe Asn Met Gly Glu Phe Cys Leu Ser Asp Leu Leu Asn Ser Asp Phe
 225 230 235 240
 Cys Asp Val Asn Glu Leu Asn Tyr Ser Asn Gly Phe Asp Ser Ser Pro
 245 250 255
 Ser Pro Asp Gln Pro Pro Met Asp Phe Ser Asp Glu Met Leu Lys Glu
 260 265 270
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 275 280 285
 Asn Leu Gln Ser Leu Pro Pro Phe Ile Glu Asn Gly Ile Glu
 290 295 300

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cg	gcac	gaga	ct	cca	aaca	atg	tcc	atg	aaa	aaa	gaa	ggt	gaa	att	cta	tac	112
						Met	Ser	Met	Lys	Lys	Glu	Gly	Glu	Ile	Leu	Tyr	
						1				5					10		
aaa	aag	gga	tta	tgg	gca	atg	gag	gaa	gac	aag	tta	ctc	att	gat	tat		160
Lys	Lys	Gly	Leu	Trp	Ala	Met	Glu	Glu	Asp	Lys	Leu	Leu	Ile	Asp	Tyr		
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Val	Asn	Val	His	Gly	Lys	Gly	Gln	Trp	Asn	Lys	Ile	Ala	Asn	Arg	Thr		
			30				35					40					
ggt	ttg	aag	aga	agt	ggg	aaa	agt	tgt	cgg	cta	agg	tgg	atg	aat	tac		256
Gly	Leu	Lys	Arg	Ser	Gly	Lys	Ser	Cys	Arg	Leu	Arg	Trp	Met	Asn	Tyr		
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Leu	Ser	Pro	Asn	Val	Lys	Lys	Gly	Asp	Phe	Ser	Glu	Glu	Glu	Glu	Asp		
	60				65				70						75		
ctc	gtc	att	aga	ctt	cat	aag	ctt	ctt	gga	aac	agg	tgg	tct	ttg	att		352
Leu	Val	Ile	Arg	Leu	His	Lys	Leu	Leu	Gly	Asn	Arg	Trp	Ser	Leu	Ile		
				80					85					90			
gcg	aaa	cga	gtt	cca	ggt	cga	act	gac	aat	caa	gtc	aag	aat	tac	tgg		400
Ala	Lys	Arg	Val	Pro	Gly	Arg	Thr	Asp	Asn	Gln	Val	Lys	Asn	Tyr	Trp		
			95					100					105				
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Asn	Ser	His	Leu	Arg	Lys	Lys	Leu	Gly	Ile	Ile	Asp	Gln	Asn	Lys	Thr		
		110					115				120						
agg	atc	gat	ttt	tgt	caa	agt	tca	aag	caa	gtc	aaa	gtg	tgt	cat	gtt		496
Arg	Ile	Asp	Phe	Cys	Gln	Ser	Ser	Lys	Gln	Val	Lys	Val	Cys	His	Val		
	125					130					135						

gat gag gca gcc acg gat cca agt cct gga cat gga aca acc act gaa	544
Asp Glu Ala Ala Thr Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu	
140 145 150 155	
acc acg ggt ata aca gtg gat cag agt aac cag cag gaa gtc att gat	592
Thr Thr Gly Ile Thr Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp	
160 165 170	
cat cgg gtc tta aac aat act act caa gaa tca atg acc agt gag agt	640
His Arg Val Leu Asn Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser	
175 180 185	
tat atc aac act ttc tgg att cct gac cat gat tat gag cta agt aca	688
Tyr Ile Asn Thr Phe Trp Ile Pro Asp His Asp Tyr Glu Leu Ser Thr	
190 195 200	
ctt gcc atg att gac cat gat tat gag cta agt aca ctt gcc atg att	736
Leu Ala Met Ile Asp His Asp Tyr Glu Leu Ser Thr Leu Ala Met Ile	
205 210 215	
gac cac ttc cat gaa tgt tct tct ttt cat ctt agc tag agactatggt	785
Asp His Phe His Glu Cys Ser Ser Phe His Leu Ser	
220 225 230	
attagattcg gggttttattt ttagatataa gtatgcatct aacatggcaa tgttaaattt	845
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<210> 8
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 <212> PRT
 <213> Gossypium hirsutum

<400> 8

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35 40 45	
Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Ser Pro Asn Val	
50 55 60	
Lys Lys Gly Asp Phe Ser Glu Glu Glu Glu Asp Leu Val Ile Arg Leu	
65 70 75 80	
His Lys Leu Leu Gly Asn Arg Trp Ser Leu Ile Ala Lys Arg Val Pro	
85 90 95	
Gly Arg Thr Asp Asn Gln Val Lys Asn Tyr Trp Asn Ser His Leu Arg	
100 105 110	
Lys Lys Leu Gly Ile Ile Asp Gln Asn Lys Thr Arg Ile Asp Phe Cys	
115 120 125	
Gln Ser Ser Lys Gln Val Lys Val Cys His Val Asp Glu Ala Ala Thr	
130 135 140	
Asp Pro Ser Pro Gly His Gly Thr Thr Thr Glu Thr Thr Gly Ile Thr	
145 150 155 160	
Val Asp Gln Ser Asn Gln Gln Glu Val Ile Asp His Arg Val Leu Asn	
165 170 175	
Asn Thr Thr Gln Glu Ser Met Thr Ser Glu Ser Tyr Ile Asn Thr Phe	
180 185 190	

Trp	Ile	Pro	Asp	His	Asp	Tyr	Glu	Leu	Ser	Thr	Leu	Ala	Met	Ile	Asp
		195					200					205			
His	Asp	Tyr	Glu	Leu	Ser	Thr	Leu	Ala	Met	Ile	Asp	His	Phe	His	Glu
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225					230										

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:degenerate
 'universal' MYB primer

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 <221> modified_base
 <222> (3)
 <223> n = g, a, c or t

<220>
 <221> modified_base
 <222> (15)
 <223> n = i

<400> 9
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20

<210> 10
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:degenerate
 'universal' MYB primer

<220>
 <221> modified_base
 <222> (17)
 <223> n = g, a, c or t

<400> 10
 srttrtctgt tckkccngg

19

<210> 11
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:highly
 conserved peptide coded by degenerate 'universal'
 MYB primer

<400> 11
Gly Lys Ser Cys Arg Leu
1 5

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly
conserved peptide coded by degenerate 'universal'
MYB primer

<400> 12
Pro Gly Arg Thr Asp Asn
1 5

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT105

<400> 13
aagcagagga attgatccac 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT106

<400> 14
accctatgaa tccaagggtc 20

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer COT107

<400> 15
cctcggaaca aattgtgcc 19

<210> 16
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
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 primer COT108

 <400> 16
 cctcggaaca aattgtgcc 19

 <210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT109

 <400> 17
 cagaaggaga aacacagagg 20

 <210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT110

 <400> 18
 gctacagttc actatgtcgg 20

 <210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT111

 <400> 19
 ccattaactc aaagcatgcc 20

 <210> 20
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 <212> DNA
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 <220>
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 primer COT112

<400> 20
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<210> 21
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT113

<400> 21
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<210> 22
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 <212> DNA
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<220>
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 primer COT114

<400> 22
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<210> 23
 <211> 20
 <212> DNA
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<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT115

<400> 23
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<210> 24
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer COT116

<400> 24
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<210> 25
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 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:conserved motif
within the basic 'transregulatory region 1' (TRR1)
domain

<220>
<221> MOD_RES
<222> (5)..(6)
<223> Xaa = any amino acid

<400> 25
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zinc-finger motif

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B1
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Cys